



# 6

SEQUENCE LISTING

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A<sup>1</sup>

<120> COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL  
STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN  
STAAU\_R9

<130> 073406-0701

<140> 10/025,222

<141> 2001-12-19

<150> 60/256,349

<151> 2000-12-19

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 1800

<212> DNA

<213> Staphylococcus aureus

<400> 1

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catgatgaaa	agacaccttc	atttacagtt	tctgaagata	aacaaatttg	tcattgtttt	180
ggttgtaaaa	aaggtggcaa	tgtttttcaa	tttactcaag	aaattaaaga	catatcattt	240
ggtgaagcgg	ttaaagaatt	aggtgataga	gttaatgttg	ctgtagatat	tgaggcaaca	300
caatctaact	caaatgttca	aattgcttct	gatgatttac	aaatgattga	aatgcatgag	360
ttaatacaag	aattttatta	ttacgcttta	acaaagacag	tcgaaggcga	acaagcatta	420
acgtacttac	agaacgtgg	ttttacagat	gcgcttatta	aagagcgagg	cattggcttt	480
gcacccgata	gtcacattt	ttgtcatgat	tttcttcaaa	aaaaggggta	cgatattgaa	540
tttagcatatg	aagccggatt	attatcacgt	aacgaagaaa	atttcagtta	ttacgataga	600
tttcgaaatc	gtattatgtt	tcctttgaaa	aatgcgcaag	gaagaattgt	tggatattca	660
ggtcgaacat	ataccgggtca	agaaccaaaa	tacttaaata	gtcctgaaac	acctatcttt	720
caaaaaagaa	agttgttata	caacttagat	aaagcgcgta	aatcaattag	aaaattagat	780
gaaatcgat	tactagaagg	ttttatggat	gttataaaat	ctgatactgc	tggcttgaaa	840
aacgttggtg	caacaatggg	tacacagttg	tcagatgaac	atattacttt	tatacgaaag	900
ttaacatcaa	atataacatt	aatgtttgat	ggggattttg	cgggtagtga	agcaacactt	960
aaaacaggtc	aaaatttggt	acagcaaggg	ctaaatgtat	ttgttataca	attgccatca	1020
ggcatggatc	cggatgaata	cattggtaag	tatggcaacg	atgcatttac	tgcttttgta	1080
aaaaatgaca	aaaagtcatt	tgcacattat	aaagtgaagta	tattaaaga	tgaaattgca	1140
cataatgacc	tttcatatga	acgttatattg	aaagaactaa	gtcatgatat	ttcgcttatg	1200
aaatcatcga	ttttgcaaca	aaaggcttta	aatgatgttg	caccattttt	caatgtagt	1260
cctgagcaat	tagctaacga	aatacaattc	aatcaagcac	cagccaatta	ttatccagaa	1320
gatgagtatg	gcggttacat	tgaacctgag	ccaattggta	tggcacaatt	tgacaatttg	1380
agccgtcaag	aaaaagcgga	gcgagcattt	ttaaaacatt	taatgagaga	taaagataca	1440
tttttaaatt	attatgaaaag	tgttgataag	gataaacttca	caaatcagca	ttttaaatat	1500
gtattcgaag	tcttacatga	tttttatgcg	gaaaatgatc	aatataatat	cagtgatgct	1560
gtgcagtatg	ttaattcaaa	tgagttgaga	gaaacactaa	ttagcttaga	acaatataat	1620
ttgaatgacg	aaccatagga	aaatgaaatt	gatgattatg	tcaatgttat	taatgaaaaa	1680
ggacaagaaa	caattgagtc	attgaatcat	aaattaaggg	aagctacaag	gattggcgat	1740
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STAPHYLOCOCCUS AUREUS

<210> 2  
 <211> 599  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 2

Leu	Arg	Ile	Asp	Gln	Ser	Ile	Ile	Asn	Glu	Ile	Lys	Asp	Lys	Thr	Asp
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Ile	Leu	Asp	Leu	Val	Ser	Glu	Tyr	Val	Lys	Leu	Glu	Lys	Arg	Gly	Arg
		20						25					30		
Asn	Tyr	Ile	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe
		35					40					45			
Thr	Val	Ser	Glu	Asp	Lys	Gln	Ile	Cys	His	Cys	Phe	Gly	Cys	Lys	Lys
	50					55						60			
Gly	Gly	Asn	Val	Phe	Gln	Phe	Thr	Gln	Glu	Ile	Lys	Asp	Ile	Ser	Phe
65					70					75					80
Val	Glu	Ala	Val	Lys	Glu	Leu	Gly	Asp	Arg	Val	Asn	Val	Ala	Val	Asp
				85					90						95
Ile	Glu	Ala	Thr	Gln	Ser	Asn	Ser	Asn	Val	Gln	Ile	Ala	Ser	Asp	Asp
			100					105						110	
Leu	Gln	Met	Ile	Glu	Met	His	Glu	Leu	Ile	Gln	Glu	Phe	Tyr	Tyr	Tyr
		115					120					125			
Ala	Leu	Thr	Lys	Thr	Val	Glu	Gly	Glu	Gln	Ala	Leu	Thr	Tyr	Leu	Gln
	130					135					140				
Glu	Arg	Gly	Phe	Thr	Asp	Ala	Leu	Ile	Lys	Glu	Arg	Gly	Ile	Gly	Phe
145					150					155					160
Ala	Pro	Asp	Ser	Ser	His	Phe	Cys	His	Asp	Phe	Leu	Gln	Lys	Lys	Gly
				165					170					175	
Tyr	Asp	Ile	Glu	Leu	Ala	Tyr	Glu	Ala	Gly	Leu	Leu	Ser	Arg	Asn	Glu
		180					185						190		
Glu	Asn	Phe	Ser	Tyr	Tyr	Asp	Arg	Phe	Arg	Asn	Arg	Ile	Met	Phe	Pro
	195						200					205			
Leu	Lys	Asn	Ala	Gln	Gly	Arg	Ile	Val	Gly	Tyr	Ser	Gly	Arg	Thr	Tyr
	210					215					220				
Thr	Gly	Gln	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	Thr	Pro	Ile	Phe
225					230					235					240
Gln	Lys	Arg	Lys	Leu	Leu	Tyr	Asn	Leu	Asp	Lys	Ala	Arg	Lys	Ser	Ile
				245					250					255	
Arg	Lys	Leu	Asp	Glu	Ile	Val	Leu	Leu	Glu	Gly	Phe	Met	Asp	Val	Ile
			260					265					270		

Lys Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr  
 275 280 285  
 Gln Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn  
 290 295 300  
 Ile Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu  
 305 310 315 320  
 Lys Thr Gly Gln Asn Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile  
 325 330 335  
 Gln Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly  
 340 345 350  
 Asn Asp Ala Phe Thr Ala Phe Val Lys Asn Asp Lys Lys Ser Phe Ala  
 355 360 365  
 His Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu  
 370 375 380  
 Ser Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met  
 385 390 395 400  
 Lys Ser Ser Ile Leu Gln Gln Lys Ala Leu Asn Asp Val Ala Pro Phe  
 405 410 415  
 Phe Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln  
 420 425 430  
 Ala Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Ile Glu  
 435 440 445  
 Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn Leu Ser Arg Gln Glu  
 450 455 460  
 Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met Arg Asp Lys Asp Thr  
 465 470 475 480  
 Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp Asn Phe Thr Asn Gln  
 485 490 495  
 His Phe Lys Tyr Val Phe Glu Val Leu His Asp Phe Tyr Ala Glu Asn  
 500 505 510  
 Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr Val Asn Ser Asn Glu  
 515 520 525  
 Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr Asn Leu Asn Asp Glu  
 530 535 540  
 Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn Val Ile Asn Glu Lys  
 545 550 555 560  
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr  
 565 570 575

Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val  
                   580                                  585                                  590

Ala Lys Asn Lys Glu Arg Met  
                   595

<210> 3  
 <211> 216  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 3  
 atgaatataa tgcaattcaa aagcttattg aaatcgatgt atgaagagac aaagcaaagc 60  
 gacccgattg tagcaaatgt atatatcgag actgggtggg cggatcaatag attggtggac 120  
 aataacgagt tatcgctttt cgatgattac gacagagttg aaaagaaaat catgaatgaa 180  
 atcaactgga agaaaacaca cattaaggag tgttaa 216

<210> 4  
 <211> 71  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 4  
 Met Asn Ile Met Gln Phe Lys Ser Leu Leu Lys Ser Met Tyr Glu Glu  
   1                  5                                  10                                  15  
 Thr Lys Gln Ser Asp Pro Ile Val Ala Asn Val Tyr Ile Glu Thr Gly  
                   20                                  25                                  30  
 Trp Ala Val Asn Arg Leu Leu Asp Asn Asn Glu Leu Ser Pro Phe Asp  
                   35                                  40                                  45  
 Asp Tyr Asp Arg Val Glu Lys Lys Ile Met Asn Glu Ile Asn Trp Lys  
                   50                                  55                                  60  
 Lys Thr His Ile Lys Glu Cys  
   65                                  70

<210> 5  
 <211> 120  
 <212> DNA  
 <213> Staphylococcus aureus

<400> 5  
 ggacaagaaa caattgagtc attgaatcat aaattaaggg aagctacaag gattggcgat 60  
 gtagaattac aaaaatacta ttacagcaa attgttgcta agaataaaga acgcatgtag 120

<210> 6  
 <211> 39  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 6  
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys Leu Arg Glu Ala Thr  
     1                    5                    10                    15  
 Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr Leu Gln Gln Ile Val  
             20                    25                    30  
 Ala Lys Asn Lys Glu Arg Met  
             35

<210> 7  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 cgcgatccc tatccttttt cattaataac attg

34

<210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 ccggaattct tgcaataga tcaatcg

27

<210> 9  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 ggaagatctc tacatgcgtt ctttatcc

28

<210> 10  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 10  
 ccggaattca tgataggttt gtgtcct

27

<210> 11  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
ccggaattcc caaaatacct aaatagtcc

29

<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
ccggaattcg cacataatga cctttca

27

<210> 13  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cgcggatcca tgccatgatgg caattg

26

<210> 14  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
ccatcgatga tttcataagc gaaatata

28

<210> 15  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 15  
ccggaattcc ctgagccaat tggatatggc 29

<210> 16  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
cgcggtatccc taagggttcaa tgtaaccgcc 30

<210> 17  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
ccggaattca aggataactt cacaaatcag 30

<210> 18  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
cgcggtatccc tacttatcaa cactttcata ata 33

<210> 19  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19  
ccggaattca gagaaacact aattagctta 30

<210> 20  
<211> 33  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 20

cgcggatccc tatctcaact catttgaatt aac

33

&lt;210&gt; 21

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 21

ccggaattcg gacaagaaac aattgagtc

29

&lt;210&gt; 22

&lt;211&gt; 581

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 22

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1				5					10					15	

Thr	Asp	Ile	Val	Asp	Leu	Ile	Asp	Ala	Arg	Val	Lys	Leu	Lys	Lys	Gln
			20					25					30		

Gly	Lys	Asn	Phe	His	Ala	Cys	Cys	Pro	Phe	His	Asn	Glu	Lys	Thr	Pro
	35						40					45			

Ser	Phe	Thr	Val	Asn	Gly	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys
	50					55					60				

Gly	Ala	His	Gly	Asn	Ala	Ile	Asp	Phe	Leu	Met	Asn	Tyr	Asp	Lys	Leu
65					70					75					80

Glu	Phe	Val	Glu	Thr	Val	Glu	Glu	Leu	Ala	Ala	Met	His	Asn	Leu	Glu
				85					90					95	

Val	Pro	Phe	Glu	Ala	Gly	Ser	Gly	Pro	Ser	Gln	Ile	Glu	Arg	His	Gln
			100					105					110		

Arg	Gln	Thr	Leu	Tyr	Gln	Leu	Met	Asp	Gly	Leu	Asn	Thr	Phe	Tyr	Gln
		115				120						125			

Gln	Ser	Leu	Gln	Gln	Pro	Val	Ala	Thr	Ser	Ala	Arg	Gln	Tyr	Leu	Glu
	130					135					140				

Lys	Arg	Gly	Leu	Ser	His	Glu	Val	Ile	Ala	Arg	Phe	Ala	Ile	Gly	Phe
145					150					155					160

Ala	Pro	Pro	Gly	Trp	Asp	Asn	Val	Leu	Lys	Arg	Phe	Gly	Gly	Asn	Pro
				165					170					175	



Glu	Asn	Arg	Gln	Ser	Leu	Ile	Asp	Ala	Gly	Met	Leu	Val	Thr	Asn	Asp	
			180					185					190			
Gln	Gly	Arg	Ser	Tyr	Asp	Arg	Phe	Arg	Glu	Arg	Val	Met	Phe	Pro	Ile	
		195					200					205				
Arg	Asp	Lys	Arg	Gly	Arg	Val	Ile	Gly	Phe	Gly	Gly	Arg	Val	Leu	Gly	
	210					215					220					
Asn	Asp	Thr	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	Thr	Asp	Ile	Phe	His	
225					230					235					240	
Lys	Gly	Arg	Gln	Leu	Tyr	Gly	Leu	Tyr	Glu	Ala	Gln	Gln	Asp	Asn	Ala	
			245						250					255		
Glu	Pro	Asn	Arg	Leu	Leu	Val	Val	Glu	Gly	Tyr	Met	Asp	Val	Val	Ala	
		260						265					270			
Leu	Ala	Gln	Tyr	Gly	Ile	Asn	Tyr	Ala	Val	Ala	Ser	Leu	Gly	Thr	Ser	
	275						280					285				
Thr	Thr	Ala	Asp	His	Ile	Gln	Leu	Leu	Phe	Arg	Ala	Thr	Asn	Asn	Val	
	290					295					300					
Ile	Cys	Cys	Tyr	Asp	Gly	Asp	Arg	Ala	Gly	Arg	Asp	Ala	Ala	Trp	Arg	
305					310					315					320	
Ala	Leu	Glu	Thr	Ala	Leu	Pro	Tyr	Met	Thr	Asp	Gly	Arg	Gln	Leu	Arg	
			325						330					335		
Phe	Met	Phe	Leu	Pro	Asp	Gly	Glu	Asp	Pro	Asp	Thr	Leu	Val	Arg	Lys	
		340						345					350			
Glu	Gly	Lys	Glu	Ala	Phe	Glu	Ala	Arg	Met	Glu	Gln	Ala	Met	Pro	Leu	
	355						360					365				
Ser	Ala	Phe	Leu	Phe	Asn	Ser	Leu	Met	Pro	Gln	Val	Asp	Leu	Ser	Thr	
	370					375					380					
Pro	Asp	Gly	Arg	Ala	Arg	Leu	Ser	Thr	Leu	Ala	Leu	Pro	Leu	Ile	Ser	
385					390					395					400	
Gln	Val	Pro	Gly	Glu	Thr	Leu	Arg	Ile	Tyr	Leu	Arg	Gln	Glu	Leu	Gly	
			405						410					415		
Asn	Lys	Leu	Gly	Ile	Leu	Asp	Asp	Ser	Gln	Leu	Glu	Arg	Leu	Met	Pro	
		420						425					430			
Lys	Ala	Ala	Glu	Ser	Gly	Val	Ser	Arg	Pro	Val	Pro	Gln	Leu	Lys	Arg	
	435						440					445				
Thr	Thr	Met	Arg	Ile	Leu	Ile	Gly	Leu	Leu	Val	Gln	Asn	Pro	Glu	Leu	
	450					455					460					
Ala	Thr	Leu	Val	Pro	Pro	Leu	Glu	Asn	Leu	Asp	Glu	Asn	Lys	Leu	Pro	
465					470					475					480	

Gly Leu Gly Leu Phe Arg Glu Leu Val Asn Thr Cys Leu Ser Gln Pro  
                             485                            490                            495

Gly Leu Thr Thr Gly Gln Leu Leu Glu His Tyr Arg Gly Thr Asn Asn  
                             500                            505                            510

Ala Ala Thr Leu Glu Lys Leu Ser Met Trp Asp Asp Ile Ala Asp Lys  
                             515                            520                            525

Asn Ile Ala Glu Gln Thr Phe Thr Asp Ser Leu Asn His Met Phe Asp  
                             530                            535                            540

Ser Leu Leu Glu Leu Arg Gln Glu Glu Leu Ile Ala Arg Glu Arg Thr  
                             545                            550                            555                            560

His Gly Leu Ser Asn Glu Glu Arg Leu Glu Leu Trp Thr Leu Asn Gln  
                             565                            570                            575

Glu Leu Ala Lys Lys  
                             580

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 23

ccgctcgagc tccaaattcc aaaacag

27

<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

cgggatccaa taagactcct ttttac

26

<210> 25

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

gcgcatctgt aaaaccacg

19

<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
 gcacgaattc aagaagaatt g 21

<210> 27  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 27  
 gatctcgtcg tgcattctgtt ggatccccgg aattccccggg 40

<210> 28  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 28  
 tcgaccggg aattccggg atccaacaga tgcacgacga 40

<210> 29  
 <211> 9  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 29  
 Tyr Tyr Leu Gln Gln Ile Val Ala Lys  
 1 5

<210> 30  
 <211> 10  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 30  
 Glu Leu Ser His Asp Ile Ser Leu Met Lys  
 1 5 10

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 31  
 Ile Asp Gln Ser Ile Ile Asn Glu Ile Lys  
 1 5 10

<210> 32  
 <211> 11  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 32  
 Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys  
 1 5 10

<210> 33  
 <211> 10  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 33  
 Asn Glu Glu Asn Phe Ser Tyr Tyr Asp Arg  
 1 5 10

<210> 34  
 <211> 12  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 34  
 Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln Lys  
 1 5 10

<210> 35  
 <211> 16  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 35  
 Lys Gly Tyr Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg  
 1 5 10 15

<210> 36  
 <211> 17  
 <212> PRT  
 <213> Staphylococcus aureus

<400> 36  
 Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser Tyr Glu  
 1 5 10 15

Arg

&lt;210&gt; 37

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: Illustrative  
zf-CHC2 comparison peptide

&lt;400&gt; 37

Ile	Pro	Glu	Glu	Ser	Ile	Asp	Glu	Leu	Lys	Asn	Arg	Ile	Asp	Ile	Val
1				5					10					15	

Asp	Val	Ile	Ser	Glu	Tyr	Val	Lys	Leu	Lys	Lys	Lys	Gly	Arg	Asn	Tyr
			20					25					30		

Lys	Gly	Leu	Cys	Pro	Phe	His	Asp	Glu	Lys	Thr	Pro	Ser	Phe	Ser	Val
	35						40					45			

Ser	Pro	Glu	Lys	Gln	Phe	Tyr	His	Cys	Phe	Gly	Cys	Gly	Ala	Gly	Gly
	50					55					60				

Asp	Ala	Ile	Lys	Phe	Leu	Met	Lys	Tyr	Glu	Lys	Leu	Ser	Phe	Val	Glu
65					70					75					80

Ala	Val	Glu	Lys	Leu	Ala	Asp	Arg	Ala	Gly	Ile	Asp	Leu	Pro	Tyr	Glu
				85					90					95	

Lys Gly

&lt;210&gt; 38

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Unknown Organism

&lt;220&gt;

<223> Description of Unknown Organism: Illustrative  
toprim comparison peptide

&lt;400&gt; 38

Lys	Val	Leu	Ile	Ile	Val	Glu	Gly	Pro	Ser	Asp	Ala	Lys	Ala	Leu	Ala
1				5					10					15	

Lys	Ala	Leu	Gly	Lys	Pro	Ser	Lys	Arg	Lys	Ile	Val	Tyr	Glu	Leu	Pro
		20						25					30		

Gly	Gly	Lys	Asp	Gly	Asn	Val	Val	Ala	Ser	Leu	Gly	His	Leu	Val	Asp
	35						40					45			

Leu	Pro	Thr	Pro	Glu	Gly	Tyr	Asp	Asp	Lys	Tyr	Lys	Trp	Leu	Trp	Leu
	50					55					60				

Pro Ile Val Asp Val Lys Lys Gly Phe Glu Pro Tyr Gln Ile Glu Phe  
65 70 75 80

Asp Gln Leu Cys Lys Cys Ser Lys Lys Ile Asp Leu Lys Lys Glu Gln  
85 90 95

Leu Lys Leu Leu Lys Lys Leu Ala Lys Lys Ala Asp Glu Val Ile Leu  
100 105 110

Ala Thr Asp Pro Asp Arg Glu Gly Glu Ala Ile Ala Trp Lys Leu Leu  
115 120 125

Glu Leu Leu Lys Pro Tyr Gly Pro Val Glu Leu Glu Asp Asp Lys Lys  
130 135 140

Val Arg Arg Ile Phe Leu Pro  
145 150

<210> 39  
<211> 572  
<212> PRT  
<213> Staphylococcus aureus

<400> 39  
Met Ile Gly Leu Cys Pro Phe His Asp Glu Lys Thr Pro Ser Phe Thr  
1 5 10 15

Val Ser Glu Asp Lys Gln Ile Cys His Cys Phe Gly Cys Lys Lys Gly  
20 25 30

Gly Asn Val Phe Gln Phe Thr Gln Glu Ile Lys Asp Ile Ser Phe Val  
35 40 45

Glu Ala Val Lys Glu Leu Gly Asp Arg Val Asn Val Ala Val Asp Ile  
50 55 60

Glu Ala Thr Gln Ser Asn Ser Asn Val Gln Ile Ala Ser Asp Asp Leu  
65 70 75 80

Gln Met Ile Glu Met His Glu Leu Ile Gln Glu Phe Tyr Tyr Tyr Ala  
85 90 95

Leu Thr Lys Thr Val Glu Gly Glu Gln Ala Leu Thr Tyr Leu Gln Glu  
100 105 110

Arg Gly Phe Thr Asp Ala Leu Ile Lys Glu Arg Gly Ile Gly Phe Ala  
115 120 125

Pro Asp Ser Ser His Phe Cys His Asp Phe Leu Gln Lys Lys Gly Tyr  
130 135 140

Asp Ile Glu Leu Ala Tyr Glu Ala Gly Leu Leu Ser Arg Asn Glu Glu  
145 150 155 160

Asn Phe Ser Tyr Tyr Asp Arg Phe Arg Asn Arg Ile Met Phe Pro Leu  
165 170 175

Lys Asn Ala Gln Gly Arg Ile Val Gly Tyr Ser Gly Arg Thr Tyr Thr  
 180 185 190  
 Gly Gln Glu Pro Lys Tyr Leu Asn Ser Pro Glu Thr Pro Ile Phe Gln  
 195 200 205  
 Lys Arg Lys Leu Leu Tyr Asn Leu Asp Lys Ala Arg Lys Ser Ile Arg  
 210 215 220  
 Lys Leu Asp Glu Ile Val Leu Leu Glu Gly Phe Met Asp Val Ile Lys  
 225 230 235 240  
 Ser Asp Thr Ala Gly Leu Lys Asn Val Val Ala Thr Met Gly Thr Gln  
 245 250 255  
 Leu Ser Asp Glu His Ile Thr Phe Ile Arg Lys Leu Thr Ser Asn Ile  
 260 265 270  
 Thr Leu Met Phe Asp Gly Asp Phe Ala Gly Ser Glu Ala Thr Leu Lys  
 275 280 285  
 Thr Gly Gln His Leu Leu Gln Gln Gly Leu Asn Val Phe Val Ile Gln  
 290 295 300  
 Leu Pro Ser Gly Met Asp Pro Asp Glu Tyr Ile Gly Lys Tyr Gly Asn  
 305 310 315 320  
 Asp Ala Phe Thr Thr Phe Val Lys Asn Asp Lys Lys Ser Phe Ala His  
 325 330 335  
 Tyr Lys Val Ser Ile Leu Lys Asp Glu Ile Ala His Asn Asp Leu Ser  
 340 345 350  
 Tyr Glu Arg Tyr Leu Lys Glu Leu Ser His Asp Ile Ser Leu Met Lys  
 355 360 365  
 Ser Ser Ile Leu Gln Gln Lys Ala Ile Asn Asp Val Ala Pro Phe Phe  
 370 375 380  
 Asn Val Ser Pro Glu Gln Leu Ala Asn Glu Ile Gln Phe Asn Gln Ala  
 385 390 395 400  
 Pro Ala Asn Tyr Tyr Pro Glu Asp Glu Tyr Gly Gly Tyr Asp Glu Tyr  
 405 410 415  
 Gly Gly Tyr Ile Glu Pro Glu Pro Ile Gly Met Ala Gln Phe Asp Asn  
 420 425 430  
 Leu Ser Arg Arg Glu Lys Ala Glu Arg Ala Phe Leu Lys His Leu Met  
 435 440 445  
 Arg Asp Lys Asp Thr Phe Leu Asn Tyr Tyr Glu Ser Val Asp Lys Asp  
 450 455 460  
 Asn Phe Thr Asn Gln His Phe Lys Tyr Val Phe Glu Val Leu His Asp  
 465 470 475 480

Phe Tyr Ala Glu Asn Asp Gln Tyr Asn Ile Ser Asp Ala Val Gln Tyr  
                                   485                                  490                                  495  
 Val Asn Ser Asn Glu Leu Arg Glu Thr Leu Ile Ser Leu Glu Gln Tyr  
                                   500                                  505                                  510  
 Asn Leu Asn Gly Glu Pro Tyr Glu Asn Glu Ile Asp Asp Tyr Val Asn  
                                   515                                  520                                  525  
 Val Ile Asn Glu Lys Gly Gln Glu Thr Ile Glu Ser Leu Asn His Lys  
                                   530                                  535                                  540  
 Leu Arg Glu Ala Thr Arg Ile Gly Asp Val Glu Leu Gln Lys Tyr Tyr  
                                   545                                  550                                  555                                  560  
 Leu Gln Gln Ile Val Ala Lys Asn Lys Glu Arg Met  
                                   565                                  570

<210> 40  
 <211> 597  
 <212> PRT  
 <213> *Geobacillus stearothermophilus*

<400> 40  
 Met Gly His Arg Ile Pro Glu Glu Thr Ile Glu Ala Ile Arg Arg Gly  
   1                                  5                                  10                                  15  
 Val Asp Ile Val Asp Val Ile Gly Glu Tyr Val Gln Leu Lys Arg Gln  
                                   20                                  25                                  30  
 Gly Arg Asn Tyr Phe Gly Leu Cys Pro Phe His Gly Glu Lys Thr Pro  
                                   35                                  40                                  45  
 Ser Phe Ser Val Ser Pro Glu Lys Gln Ile Phe His Cys Phe Gly Cys  
                                   50                                  55                                  60  
 Gly Ala Gly Gly Asn Ala Phe Thr Phe Leu Met Asp Ile Glu Gly Ile  
                                   65                                  70                                  75                                  80  
 Pro Phe Val Glu Ala Ala Lys Arg Leu Ala Ala Lys Ala Gly Val Asp  
                                   85                                  90                                  95  
 Leu Ser Val Tyr Glu Leu Asp Val Arg Gly Arg Asp Asp Gly Gln Thr  
                                   100                                  105                                  110  
 Asp Glu Ala Lys Ala Met Thr Glu Ala His Ala Leu Leu Lys Arg Phe  
                                   115                                  120                                  125  
 Tyr His His Leu Leu Val His Thr Lys Glu Gly Gln Ala Ala Leu Asp  
                                   130                                  135                                  140  
 Tyr Leu Gln Ala Arg Gly Trp Thr Lys Glu Thr Ile Asp Arg Phe Glu  
                                   145                                  150                                  155                                  160  
 Ile Gly Tyr Ala Pro Asp Ala Pro Asp Ala Ala Ala Lys Leu Leu Glu  
                                   165                                  170                                  175



Ser His Ser Phe Ser Leu Pro Val Met Glu Lys Ala Gly Leu Leu Thr  
 180 185 190  
 Lys Lys Glu Asp Gly Arg Tyr Val Gly Arg Phe Arg Asn Arg Ile Met  
 195 200 205  
 Phe Pro Ile His Asp His Arg Gly Glu Thr Val Gly Phe Ser Gly Arg  
 210 215 220  
 Leu Leu Gly Glu Gly His Pro Lys Tyr Val Asn Ser Pro Glu Thr Pro  
 225 230 235 240  
 Val Phe Arg Lys Gly Ala Ile Leu Tyr His Phe His Ala Ala Arg Val  
 245 250 255  
 Pro Ile Arg Lys Arg Gln Glu Ala Leu Leu Val Glu Gly Phe Ala Asp  
 260 265 270  
 Val Ile Ser Ala Ala Gln Ala Gly Ile Asp Tyr Ala Ile Ala Thr Met  
 275 280 285  
 Gly Thr Ser Leu Thr Glu Glu Gln Ala Arg Ile Leu Arg Pro Cys Asp  
 290 295 300  
 Thr Ile Thr Ile Cys Tyr Asp Gly Asp Arg Ala Gly Ile Glu Ala Ala  
 305 310 315 320  
 Trp Ala Ala Ala Glu Gln Leu Ser Ala Leu Gly Cys Arg Val Lys Val  
 325 330 335  
 Ala Ser Leu Pro Asn Gly Leu Asp Pro Asp Glu Tyr Ile Arg Val Tyr  
 340 345 350  
 Gly Gly Glu Arg Phe Ala Gly Glu Ala Gly Cys Arg Arg Pro Leu Val  
 355 360 365  
 Ala Phe Lys Met Ala Tyr Leu Arg Arg Gly Lys Asn Leu Gln His Glu  
 370 375 380  
 Gly Glu Arg Leu Arg Tyr Ile Asp Glu Ala Leu Arg Glu Ile Gly Lys  
 385 390 395 400  
 Leu Ser Ser Pro Val Glu Gln Asp Tyr Tyr Leu Arg Gln Leu Ala Glu  
 405 410 415  
 Glu Phe Ser Leu Ser Leu Ser Ala Leu His Glu Gln Leu Ser Arg Ser  
 420 425 430  
 Gln Arg Glu Arg Thr Lys Pro Arg Glu Ala Pro Asp Gly Glu Thr Ala  
 435 440 445  
 Arg Pro Met Leu Ala Lys Lys Leu Leu Pro Ala Phe Gln Asn Ala Glu  
 450 455 460  
 Arg Leu Leu Leu Ala His Met Met Arg Ser Arg Asp Val Ala Leu Val  
 465 470 475 480

Val Gln Glu Arg Ile Gly Gly Arg Phe Asn Ile Glu Glu His Arg Ala  
                                   485                                  490                                  495

Leu Ala Ala Tyr Ile Tyr Ala Phe Tyr Glu Glu Gly His Glu Ala Asp  
                                   500                                  505                                  510

Pro Gly Ala Leu Ile Ser Arg Ile Pro Gly Glu Leu Gln Pro Leu Ala  
                                   515                                  520                                  525

Ser Asp Val Ser Leu Leu Leu Ile Ala Asp Asp Val Ser Glu Gln Glu  
                                   530                                  535                                  540

Leu Glu Asp Tyr Ile Arg His Val Leu Asn Arg Pro Lys Trp Leu Met  
                                   545                                  550                                  555                                  560

Leu Lys Val Lys Glu Gln Glu Lys Thr Glu Ala Glu Arg Arg Lys Asp  
                                   565                                  570                                  575

Phe Leu Thr Ala Ala Arg Ile Ala Lys Glu Met Ile Glu Met Lys Lys  
                                   580                                  585                                  590

Met Leu Ser Ser Ser  
                                   595

<210> 41

<211> 603

<212> PRT

<213> Bacillus subtilis

<400> 41

Met Gly Asn Arg Ile Pro Asp Glu Ile Val Asp Gln Val Gln Lys Ser  
   1                                  5                                  10                                  15

Ala Asp Ile Val Glu Val Ile Gly Asp Tyr Val Gln Leu Lys Lys Gln  
                                   20                                  25                                  30

Gly Arg Asn Tyr Phe Gly Leu Cys Pro Phe His Gly Glu Ser Thr Pro  
                                   35                                  40                                  45

Ser Phe Ser Val Ser Pro Asp Lys Gln Ile Phe His Cys Phe Gly Cys  
                                   50                                  55                                  60

Gly Ala Gly Gly Asn Val Phe Ser Phe Leu Arg Gln Met Glu Gly Tyr  
                                   65                                  70                                  75                                  80

Ser Phe Ala Glu Ser Val Ser His Leu Ala Asp Lys Tyr Gln Ile Asp  
                                   85                                  90                                  95

Phe Pro Asp Asp Ile Thr Val His Ser Gly Ala Arg Pro Glu Ser Ser  
                                   100                                  105                                  110

Gly Glu Gln Lys Met Ala Glu Ala His Glu Leu Leu Lys Lys Phe Tyr  
                                   115                                  120                                  125

His His Leu Leu Ile Asn Thr Lys Glu Gly Gln Glu Ala Leu Asp Tyr  
                                   130                                  135                                  140

Leu Leu Ser Arg Gly Phe Thr Lys Glu Leu Ile Asn Glu Phe Gln Ile  
 145 150 155 160  
 Gly Tyr Ala Leu Asp Ser Trp Asp Phe Ile Thr Lys Phe Leu Val Lys  
 165 170 175  
 Arg Gly Phe Ser Glu Ala Gln Met Glu Lys Ala Gly Leu Leu Ile Arg  
 180 185 190  
 Arg Glu Asp Gly Ser Gly Tyr Phe Asp Arg Phe Arg Asn Arg Val Met  
 195 200 205  
 Phe Pro Ile His Asp His His Gly Ala Val Val Ala Phe Ser Gly Arg  
 210 215 220  
 Ala Leu Gly Ser Gln Gln Pro Lys Tyr Met Asn Ser Pro Glu Thr Pro  
 225 230 235 240  
 Leu Phe His Lys Ser Lys Leu Leu Tyr Asn Phe Tyr Lys Ala Arg Leu  
 245 250 255  
 His Ile Arg Lys Gln Glu Arg Ala Val Leu Phe Glu Gly Phe Ala Asp  
 260 265 270  
 Val Tyr Thr Ala Val Ser Ser Asp Val Lys Glu Ser Ile Ala Thr Met  
 275 280 285  
 Gly Thr Ser Leu Thr Asp Asp His Val Lys Ile Leu Arg Arg Asn Val  
 290 295 300  
 Glu Glu Ile Ile Leu Cys Tyr Asp Ser Asp Lys Ala Gly Tyr Glu Ala  
 305 310 315 320  
 Thr Leu Lys Ala Ser Glu Leu Leu Gln Lys Lys Gly Cys Lys Val Arg  
 325 330 335  
 Val Ala Met Ile Pro Asp Gly Leu Asp Pro Asp Asp Tyr Ile Lys Lys  
 340 345 350  
 Phe Gly Gly Glu Lys Phe Lys Asn Asp Ile Ile Asp Ala Ser Val Thr  
 355 360 365  
 Val Met Ala Phe Lys Met Gln Tyr Phe Arg Lys Gly Lys Asn Leu Ser  
 370 375 380  
 Asp Glu Gly Asp Arg Leu Ala Tyr Ile Lys Asp Val Leu Lys Glu Ile  
 385 390 395 400  
 Ser Thr Leu Ser Gly Ser Leu Glu Gln Glu Val Tyr Val Lys Gln Leu  
 405 410 415  
 Ala Ser Glu Phe Ser Leu Ser Gln Glu Ser Leu Thr Glu Gln Leu Ser  
 420 425 430  
 Val Phe Ser Lys Gln Asn Lys Pro Ala Asp Asn Ser Gly Glu Thr Lys  
 435 440 445

Thr Arg Arg Ala His Leu Thr Thr Lys Ala Arg Gln Lys Arg Leu Arg  
450 455 460

Pro Ala Tyr Glu Asn Ala Glu Arg Leu Leu Leu Ala His Met Leu Arg  
465 470 475 480

Asp Arg Ser Val Ile Lys Lys Val Ile Asp Arg Val Gly Phe Gln Phe  
485 490 495

Asn Ile Asp Glu His Arg Ala Leu Ala Ala Tyr Leu Tyr Ala Phe Tyr  
500 505 510

Glu Glu Gly Ala Glu Leu Thr Pro Gln His Leu Met Ala Arg Val Thr  
515 520 525

Asp Asp His Ile Ser Gln Leu Leu Ser Asp Ile Leu Met Leu Gln Val  
530 535 540

Asn Gln Glu Leu Ser Glu Ala Glu Leu Ser Asp Tyr Val Lys Lys Val  
545 550 555 560

Leu Asn Gln Arg Asn Trp Ser Met Ile Lys Glu Lys Glu Ala Glu Arg  
565 570 575

Ala Glu Ala Glu Arg Gln Lys Asp Phe Leu Arg Ala Ala Ser Leu Ala  
580 585 590

Gln Glu Ile Val Thr Leu Asn Arg Ser Leu Lys  
595 600

A<sup>v</sup>  
cont.